34. A method of genotyping comprising the steps of:

(a) obtaining nucleic acid material;

(b) amplifying a short tandem repeat polymorphism of the material to produce a signal;

(c) analyzing the signal using a linear model represented in a computing device with a memory; and

(d) identifying an allele of the polymorphism.

37. A method as described in Claim 34 wherein after the identifying step, there is the step of identifying an individual using the allele of the polymorphism in the individual's nucleic acid material.

38. A method as described in Claim 34 wherein after the identifying step, there is the step of comparing the allele with another allele.

The claims of record 39-49 are added as follows:

39. A method as described in Claim 34 wherein the analyzing step includes a method of least squares.

40. A method as described in Claim 34 wherein the analyzing step includes a maximum likelihood estimate.

41. A method as described in Claim 34 wherein the analyzing step implements the linear model using a matrix equation.

42. A method as described in Claim 41 wherein the matrix equation compares the signal with a genotype.

43. A method as described in Claim 34 wherein the identifying step includes a deconvolution of the data to produce an allele.

44. A method as described in Claim 34 wherein the nucleic acid material includes DNA from a plurality of individuals.

45. A method as described in Claim 34 wherein after the identifying step there is the step of calibrating PCR stutter.

46. A method as described in Claim 34 wherein after the producing step there is the step of diagnosing a risk of genetic disease in the individual.

47. A method as described in Claim 34 wherein after the identifying step there is the step of constructing a genetic map using the alleles.

48. A method as described in Claim 34 wherein after the identifying step there is the step of mapping a genetic trait using the alleles.

49. A method as described in Claim 34 wherein after the identifying step there is the step of positionally cloning a disease gene using the alleles.